SEQUENCE LISTING

<110> Geigenberger, Peter
Langer, Anke
Vigeolas, Helene
Stitt Nigel, Marc
van Dongen, Joost T.
Udvardi, Michael

<120> METHOD FOR ALTERING THE CONTENT OF RESERVE SUBSTANCES IN PLANTS

<130> 13311-00008-US

<150> PCT/EP2003/014774
<151> 2003-12-23

<150> DE 102 60 707.9
<151> 2002-12-23

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<170> PatentIn version 3.3

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aca ttc aag aaa aac ctt cct acc aac agt gtt ttg ttc tac acc gtt    96
Thr Phe Lys Lys Asn Leu Pro Thr Asn Ser Val Leu Phe Tyr Thr Val
            20                  25                  30

ata ttg gag ata gca cca act gca aaa gac atg ttc tcc ttt cta aag   144
Ile Leu Glu Ile Ala Pro Thr Ala Lys Asp Met Phe Ser Phe Leu Lys
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gag tct ggg cct aag cat agt cct cag ctc cag gcc cat gct gaa aag   192
Glu Ser Gly Pro Lys His Ser Pro Gln Leu Gln Ala His Ala Glu Lys
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gtt ttt gca ctg act cgt gat gct gcc act caa ctc gta gca aaa gga   240
Val Phe Ala Leu Thr Arg Asp Ala Ala Thr Gln Leu Val Ala Lys Gly
65                  70                  75                  80

gaa gtg aca ctt gca gat gcc agc tta ggt gct gtc cac gtt cag aaa   288
Glu Val Thr Leu Ala Asp Ala Ser Leu Gly Ala Val His Val Gln Lys
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gcc gtt act gat cct cat ttc gtg gtg gtt aaa gaa gcc ctg ctt caa   336
Ala Val Thr Asp Pro His Phe Val Val Val Lys Glu Ala Leu Leu Gln
            100                 105                 110

aca gta aag gaa gca gtt ggg gcg gac gaa tgg agt gat gac ttg agc   384
Thr Val Lys Glu Ala Val Gly Ala Asp Glu Trp Ser Asp Asp Leu Ser
        115                 120                 125

acc gct tgg gaa gga gca tat gat gga cta gca act gca att aag aag   432
Thr Ala Trp Glu Gly Ala Tyr Asp Gly Leu Ala Thr Ala Ile Lys Lys
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Ile Leu Glu Ile Ala Pro Thr Ala Lys Asp Met Phe Ser Phe Leu Lys
        35                  40                  45

Glu Ser Gly Pro Lys His Ser Pro Gln Leu Gln Ala His Ala Glu Lys
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Val Phe Ala Leu Thr Arg Asp Ala Ala Thr Gln Leu Val Ala Lys Gly
65                  70                  75                  80

Glu Val Thr Leu Ala Asp Ala Ser Leu Gly Ala Val His Val Gln Lys
                85                  90                  95

Ala Val Thr Asp Pro His Phe Val Val Val Lys Glu Ala Leu Leu Gln
            100                 105                 110

Thr Val Lys Glu Ala Val Gly Ala Asp Glu Trp Ser Asp Asp Leu Ser
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gta gtg aag tct tgg agt gtc atg aag aaa aac tca gct gaa tta ggt    96
Val Val Lys Ser Trp Ser Val Met Lys Lys Asn Ser Ala Glu Leu Gly
            20                  25                  30

ctc aaa ctc ttc atc aag atc ttt gag att gca cca aca acg aag aag   144
Leu Lys Leu Phe Ile Lys Ile Phe Glu Ile Ala Pro Thr Thr Lys Lys
        35                  40                  45

atg ttc tct ttc ttg aga gac tca cca att cct gct gag caa aat cca   192
Met Phe Ser Phe Leu Arg Asp Ser Pro Ile Pro Ala Glu Gln Asn Pro
    50                  55                  60

aag ctc aag cct cac gca atg tct gtt ttt gtc atg tgt tgt gaa tca   240
Lys Leu Lys Pro His Ala Met Ser Val Phe Val Met Cys Cys Glu Ser
65                  70                  75                  80

gca gta caa ctg agg aaa aca ggg aaa gtt acg gtg agg gag act act   288
Ala Val Gln Leu Arg Lys Thr Gly Lys Val Thr Val Arg Glu Thr Thr
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ttg aag aga ctt gga gcc agc cat tct aaa tac ggt gtc gtt gac gaa   336
Leu Lys Arg Leu Gly Ala Ser His Ser Lys Tyr Gly Val Val Asp Glu
            100                 105                 110

cac ttt gag gtg gcc aag tat gca ttg ttg gag acg ata aag gag gca   384
His Phe Glu Val Ala Lys Tyr Ala Leu Leu Glu Thr Ile Lys Glu Ala
        115                 120                 125

gtg ccg gag atg tgg tca ccg gag atg aag gtg gct tgg ggt cag gct   432
Val Pro Glu Met Trp Ser Pro Glu Met Lys Val Ala Trp Gly Gln Ala
    130                 135                 140

tat gat cac ctt gtt gct gcc att aaa gct gaa atg aat ctt tcc aac   480
Tyr Asp His Leu Val Ala Ala Ile Lys Ala Glu Met Asn Leu Ser Asn
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Leu Lys Leu Phe Ile Lys Ile Phe Glu Ile Ala Pro Thr Thr Lys Lys
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Met Phe Ser Phe Leu Arg Asp Ser Pro Ile Pro Ala Glu Gln Asn Pro
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Lys Leu Lys Pro His Ala Met Ser Val Phe Val Met Cys Cys Glu Ser
65                  70                  75                  80

Ala Val Gln Leu Arg Lys Thr Gly Lys Val Thr Val Arg Glu Thr Thr
                85                  90                  95

Leu Lys Arg Leu Gly Ala Ser His Ser Lys Tyr Gly Val Val Asp Glu
            100                 105                 110

His Phe Glu Val Ala Lys Tyr Ala Leu Leu Glu Thr Ile Lys Glu Ala
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Val Pro Glu Met Trp Ser Pro Glu Met Lys Val Ala Trp Gly Gln Ala
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tcg tgg gag ata ctg aaa caa gac atc ccc aaa tac agc ctt cac ttc    96
Ser Trp Glu Ile Leu Lys Gln Asp Ile Pro Lys Tyr Ser Leu His Phe
            20                  25                  30

ttc tca cag ata ctg gag ata gca cca gca gca aaa ggc ttg ttc tct   144
Phe Ser Gln Ile Leu Glu Ile Ala Pro Ala Ala Lys Gly Leu Phe Ser
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ttc cta aga gac tca gat gaa gtc cct cac aac aat cct aaa ctc aaa   192
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gct cat gct gtt aaa gtc ttc aag atg aca tgt gaa aca gct ata cag   240
Ala His Ala Val Lys Val Phe Lys Met Thr Cys Glu Thr Ala Ile Gln
65                  70                  75                  80

ctg agg gag gaa gga aag gtg gta gtg gct gac aca acc ctc caa tat   288
Leu Arg Glu Glu Gly Lys Val Val Val Ala Asp Thr Thr Leu Gln Tyr
                85                  90                  95

tta ggc tca att cat ctc aaa agc ggc gtt att gac cct cac ttc gag   336
Leu Gly Ser Ile His Leu Lys Ser Gly Val Ile Asp Pro His Phe Glu
            100                 105                 110

gtg gtg aaa gaa gct ttg cta agg aca ttg aaa gag ggg ttg ggg gag   384
Val Val Lys Glu Ala Leu Leu Arg Thr Leu Lys Glu Gly Leu Gly Glu
        115                 120                 125

aaa tac aat gaa gaa gtg gaa ggt gct tgg tct caa gct tat gat cac   432
Lys Tyr Asn Glu Glu Val Glu Gly Ala Trp Ser Gln Ala Tyr Asp His
    130                 135                 140

ttg gct tta gcc atc aag acc gag atg aaa caa gaa gag tca taa     477
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Phe Ser Gln Ile Leu Glu Ile Ala Pro Ala Ala Lys Gly Leu Phe Ser
        35                  40                  45

Phe Leu Arg Asp Ser Asp Glu Val Pro His Asn Asn Pro Lys Leu Lys
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Ala His Ala Val Lys Val Phe Lys Met Thr Cys Glu Thr Ala Ile Gln
65                  70                  75                  80

Leu Arg Glu Glu Gly Lys Val Val Val Ala Asp Thr Thr Leu Gln Tyr
                85                  90                  95

Leu Gly Ser Ile His Leu Lys Ser Gly Val Ile Asp Pro His Phe Glu
            100                 105                 110

Val Val Lys Glu Ala Leu Leu Arg Thr Leu Lys Glu Gly Leu Gly Glu
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<110> Max-Planck-Gesellschaft

<120> Method for modifying the storage reserve content in plants

<130> NAE 737/02 PCT

<150> DE 10260707.9
<151> 2002-12-23

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<170> PatentIn version 3.2

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aca ttc aag aaa aac ctt cct acc aac agt gtt ttg ttc tac acc gtt
96
Thr Phe Lys Lys Asn Leu Pro Thr Asn Ser Val Leu Phe Tyr Thr Val
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ata ttg gag ata gca cca act gca aaa gac atg ttc tcc ttt cta aag
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Ile Leu Glu Ile Ala Pro Thr Ala Lys Asp Met Phe Ser Phe Leu Lys
35 40 45

gag tct ggg cct aag cat agt cct cag ctc cag gcc cat gct gaa aag
192
Glu Ser Gly Pro Lys His Ser Pro Gln Leu Gln Ala His Ala Glu Lys
50 55 60

gtt ttt gca ctg act cgt gat gct gcc act caa ctc gta gca aaa gga
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Val Phe Ala Leu Thr Arg Asp Ala Ala Thr Gln Leu Val Ala Lys Gly
65 70 75 80

gaa gtg aca ctt gca gat gcc agc tta ggt gct gtc cac gtt cag aaa
288
Glu Val Thr Leu Ala Asp Ala Ser Leu Gly Ala Val His Val Gln Lys
85 90 95

gcc gtt act gat cct cat ttc gtg gtg gtt aaa gaa gcc ctg ctt caa
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Ala Val Thr Asp Pro His Phe Val Val Val Lys Glu Ala Leu Leu Gln
100 105 110

aca gta aag gaa gca gtt ggg gcg gac gaa tgg agt gat gac ttg agc
384
Thr Val Lys Glu Ala Val Gly Ala Asp Glu Trp Ser Asp Asp Leu Ser
115 120 125

acc gct tgg gaa gga gca tat gat gga cta gca act gca att aag aag
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Thr Ala Trp Glu Gly Ala Tyr Asp Gly Leu Ala Thr Ala Ile Lys Lys
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Ala Met Gly
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Glu Ser Gly Pro Lys His Ser Pro Gln Leu Gln Ala His Ala Glu Lys
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Val Phe Ala Leu Thr Arg Asp Ala Ala Thr Gln Leu Val Ala Lys Gly
65 70 75 80

Glu Val Thr Leu Ala Asp Ala Ser Leu Gly Ala Val His Val Gln Lys
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Ala Val Thr Asp Pro His Phe Val Val Val Lys Glu Ala Leu Leu Gln
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Val Val Lys Ser Trp Ser Val Met Lys Lys Asn Ser Ala Glu Leu Gly
20 25 30

ctc aaa ctc ttc atc aag atc ttt gag att gca cca aca acg aag aag
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Leu Lys Leu Phe Ile Lys Ile Phe Glu Ile Ala Pro Thr Thr Lys Lys
35 40 45

atg ttc tct ttc ttg aga gac tca cca att cct gct gag caa aat cca
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Met Phe Ser Phe Leu Arg Asp Ser Pro Ile Pro Ala Glu Gln Asn Pro
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Lys Leu Lys Pro His Ala Met Ser Val Phe Val Met Cys Cys Glu Ser
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Ala Val Gln Leu Arg Lys Thr Gly Lys Val Thr Val Arg Glu Thr Thr
85 90 95

ttg aag aga ctt gga gcc agc cat tct aaa tac ggt gtc gtt gac gaa
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Leu Lys Arg Leu Gly Ala Ser His Ser Lys Tyr Gly Val Val Asp Glu
100 105 110

cac ttt gag gtg gcc aag tat gca ttg ttg gag acg ata aag gag gca
384
His Phe Glu Val Ala Lys Tyr Ala Leu Leu Glu Thr Ile Lys Glu Ala
115 120 125

gtg ccg gag atg tgg tca ccg gag atg aag gtg gct tgg ggt cag gct
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Val Pro Glu Met Trp Ser Pro Glu Met Lys Val Ala Trp Gly Gln Ala
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Lys Leu Lys Pro His Ala Met Ser Val Phe Val Met Cys Cys Glu Ser
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Ala Val Gln Leu Arg Lys Thr Gly Lys Val Thr Val Arg Glu Thr Thr
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Leu Lys Arg Leu Gly Ala Ser His Ser Lys Tyr Gly Val Val Asp Glu
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His Phe Glu Val Ala Lys Tyr Ala Leu Leu Glu Thr Ile Lys Glu Ala
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tcg tgg gag ata ctg aaa caa gac atc ccc aaa tac agc ctt cac ttc
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Ser Trp Glu Ile Leu Lys Gln Asp Ile Pro Lys Tyr Ser Leu His Phe
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Phe Ser Gln Ile Leu Glu Ile Ala Pro Ala Ala Lys Gly Leu Phe Ser
35 40 45

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Phe Leu Arg Asp Ser Asp Glu Val Pro His Asn Asn Pro Lys Leu Lys
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240
Ala His Ala Val Lys Val Phe Lys Met Thr Cys Glu Thr Ala Ile Gln
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ctg agg gag gaa gga aag gtg gta gtg gct gac aca acc ctc caa tat
288
Leu Arg Glu Glu Gly Lys Val Val Val Ala Asp Thr Thr Leu Gln Tyr
85 90 95

tta ggc tca att cat ctc aaa agc ggc gtt att gac cct cac ttc gag
336
Leu Gly Ser Ile His Leu Lys Ser Gly Val Ile Asp Pro His Phe Glu
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gtg gtg aaa gaa gct ttg cta agg aca ttg aaa gag ggg ttg ggg gag
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Val Val Lys Glu Ala Leu Leu Arg Thr Leu Lys Glu Gly Leu Gly Glu
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aaa tac aat gaa gaa gtg gaa ggt gct tgg tct caa gct tat gat cac
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Lys Tyr Asn Glu Glu Val Glu Gly Ala Trp Ser Gln Ala Tyr Asp His
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Ser Trp Glu Ile Leu Lys Gln Asp Ile Pro Lys Tyr Ser Leu His Phe
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35 40 45

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Phe Leu Arg Asp Ser Asp Glu Val Pro His Asn Asn Pro Lys Leu Lys
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65          70          75          80

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         85          90          95

Leu Gly Ser Ile His Leu Lys Ser Gly Val Ile Asp Pro His Phe Glu
      100         105         110

Val Val Lys Glu Ala Leu Leu Arg Thr Leu Lys Glu Gly Leu Gly Glu
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Lys Tyr Asn Glu Glu Val Glu Gly Ala Trp Ser Gln Ala Tyr Asp His
  130         135         140

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